

09033662 030399

ATGAGAAGGTGTAGAATAAGTGGGAGGCCCCCGGCGCCCCCGGTGTCCCCGCCAGGCC  
MetArgArgCysArgIleSerGlyArgProProAlaProProGlyValProAlaGlnAla  
CCTGTCTCCCAGCCTGATGCCCTGGCCACCAGAGGAAAGTGGTGTTCATGGATAGATGTG  
ProValSerGlnProAspAlaProGlyHisGlnArgLysValValSerTrpIleAspVal  
TATACTCGCGCTACCTGCCAGCCCCGGGAGGTGGTGGTGGCCCTTGACTGTGGAGCTCATG  
TyrThrArgAlaThrCysGlnProArgGluValValValProLeuThrValGluLeuMet  
GGCACCGTGGCCAAACAGCTGGTGGCCAGCTGCGTGAAGTGTGCAGCGCTGTGGTGGCTGC  
GlyThrValAlaLysGlnLeuValProSerCysValThrValGlnArgCysGlyGlyCys  
TGCCCTGACGATGGCCTGGAGTGTGTGCCCACTGGGCAGCACCAAGTCCGGATGCAGATC  
CysProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMetGlnIle  
CTCATGATCCGGTACCCGAGCAGTCAGCTGGGGGAGATGTCCCTGGAAGAACACAGCCAG  
LeuMetIleArgTyrProSerSerGlnLeuGlyGluMetSerLeuGluGluHisSerGln  
TGTGAATGCAGACCTAAAAAAGGACAGTGTGTGAAGCCAGACAGGGCTGCTACTCCC  
CysGluCysArgProLysLysLysAspSerAlaValLysProAspArgAlaAlaThrPro  
CACCACCGTCCCCAGCCCCGTTCTGTTCGGGGCTGGGACTCTGCCCCCGGAGCACCCCTCC  
HisHisArgProGlnProArgSerValProGlyTrpAspSerAlaProGlyAlaProSer  
CCAGCTGACATACCCCAATCCCACTCCAGCCCCAGGCCCTCTGCCCACGCTGCACCCAG  
ProAlaAspIleThrGlnSerHisSerSerProArgProLeuCysProArgCysThrGln  
CACCACCAGTGCCCTGACCCCCGGACCTGCCGCTGCCGCTGTGACGCGCGAGCTTCCTC  
HisHisGlnCysProAspProArgThrCysArgCysArgCysArgArgArgSerPheLeu  
CGTTGTCAAGGGCGGGGCTTAGAGCTCAACCCAGACACCTGCAGGTGCCGGAAGCTGCGA  
ArgCysGlnGlyArgGlyLeuGluLeuAsnProAspThrCysArgCysArgLysLeuArg  
AGGTGA  
ArgEnd

FIGURE

1

1/1

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      10      20      30      40      50
MNFLLSVHWSLALLLYLHAKWSQAAPMAEGGQNH-EVVKFMDVYQRSYC
      ::||::: ::::|: :||::||| |:|
      MRRCRISGRPPAPPGVPAQAFVSQPDAPGHQRKVVSVIDVYTRATC

      60      70      80      90     100     110
HPIETLVDFIQEYPDEIEYIFKPPSCVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPH
:| |::| :| :::: :| ||::: ||||| :||| ||||::: :| ||::| :| :
QPREVVVPLTVELMGTVAQLVPSCVTVQRCGGCCPDDGLECVPTGQHQVRMQILMIR-Y

      120     130           140     150     160
QGQHIGEMSFLQHNKCECRPKK-----DRA-----RQEKKSVRGKGGQKRKRKKSRY
:: :|||: :||: ||||| ||| ||: |||: :::: :| :
PSSQLGEMSLEHSQCECRPKKKDSAVKPDRAATPHHRPQPRSVFGWDSAPGAPSPADIT

      170     180     190     200     210
KWSVPCGPCSERRKHLFVQDPQTCKCCKNTD-SRCKARQLELNERTCRCDKPRR
:| | | | :| :||: ||: ||: :| :| ||| ||| | |
QSHSSPRPLCPFRCTQHHQCPDPRTCRCRCRRRSFLRCQGRGLELNPDTCRCRKLRR

```

Figure 2. Sequence alignment of VEGF3(lower line) compared to VEGF from human (upper line).

FIGURE 2 1/1

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